From:	Carol Woody
To:	Phil_Brna@fws.gov; North, Phil
Cc:	David Chambers
Subject:	Coho Study
Date:	Friday, March 22, 2013 6:32:08 PM
Attachments:	SWIM2013FINAL.pptx.pdf

Hello Phil B. and Phil N.,

Thought you might be interested in study results I presented at the recent SWIM meeting in Dillingham, few Federal employees attended due to sequestration.

Bottom line: I analyzed genetic data (samples run by USFWS) for 5 Bristol Bay coho populations including S. Fork Koktuli and Upper Talarik Ck.
All surveyed populations were genetically distinct and results highly significant. I also sampled and compared age and size at maturity, an adaptive life history trait, between S. Fork Koktuli and U. Talarik Creek adult coho and differences in these traits were also highly significant. Results from my analysis agree with other Alaskan coho genetic studies by Olsen et al.(2003, 2004, 2011) of the USFWS Conservation genetics Lab, that indicate Alaskan coho spawning populations tend to be small, show high degrees of populations structuring, and spawning populations are genetically unique. Relative to other studied species (Chinook, chum) coho are more vulnerable to loss of significant genetic diversity due to habitat loss and/or alteration from proposed development of a mine district in Bristol Bay.

Comments criticism welcome.
Please forward to any other potentially interested agency (e.g., NOAA & EPA) types.
I will forward the manuscript that I submit to Molecular Ecology.

If there is interest in my presenting this information to a group or groups I am happy to do so.

Sincerely,

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Coho Salmon Spawning Distribution and Biodiversity in a Proposed Mining District, Bristol Bay, AK

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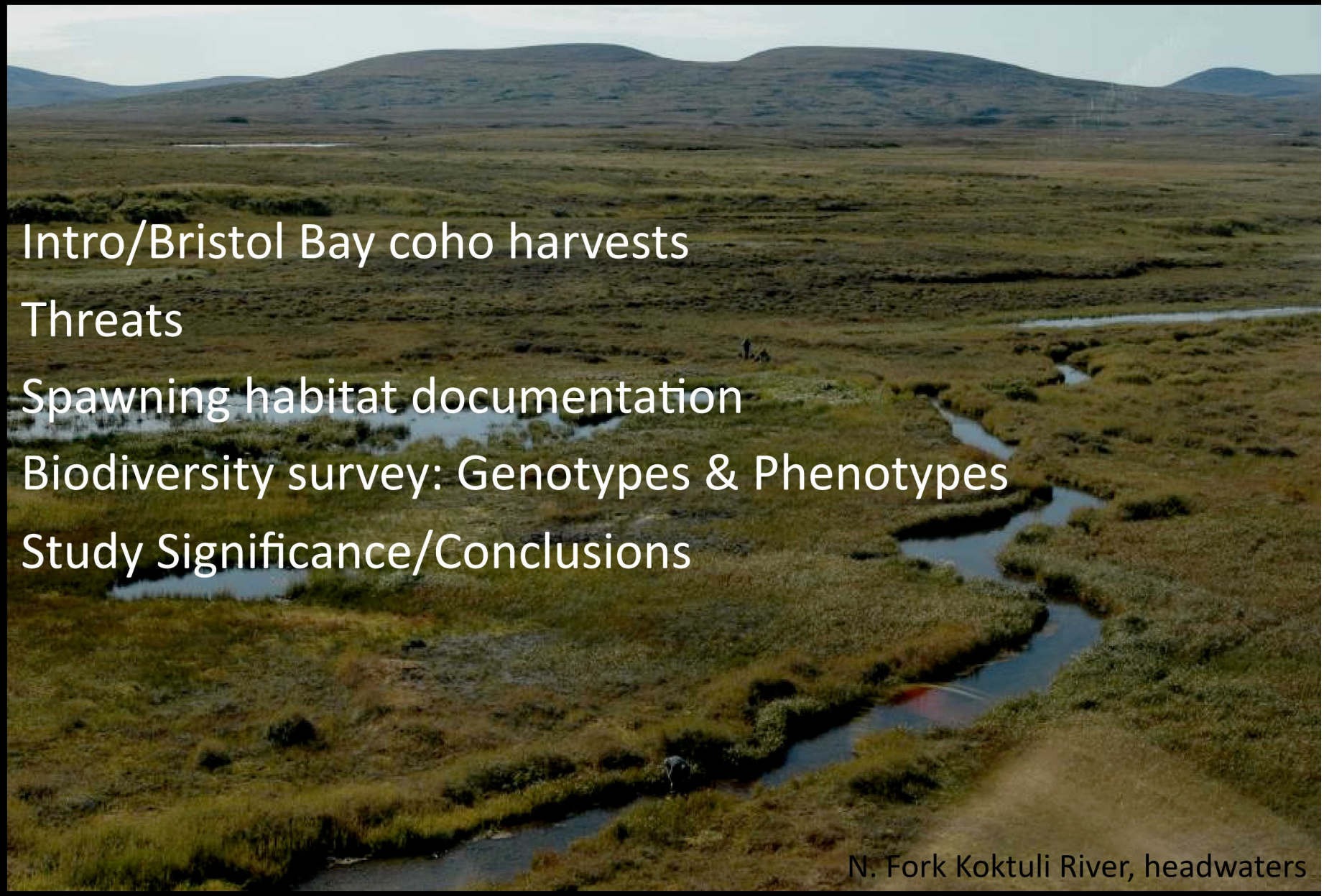
Outline

- Intro/Bristol Bay coho harvests
- Threats
- Spawning habitat documentation
- Biodiversity survey: Genotypes & Phenotypes
- Study Significance/Conclusions



N. Fork Koktuli River, headwaters

Coho salmon

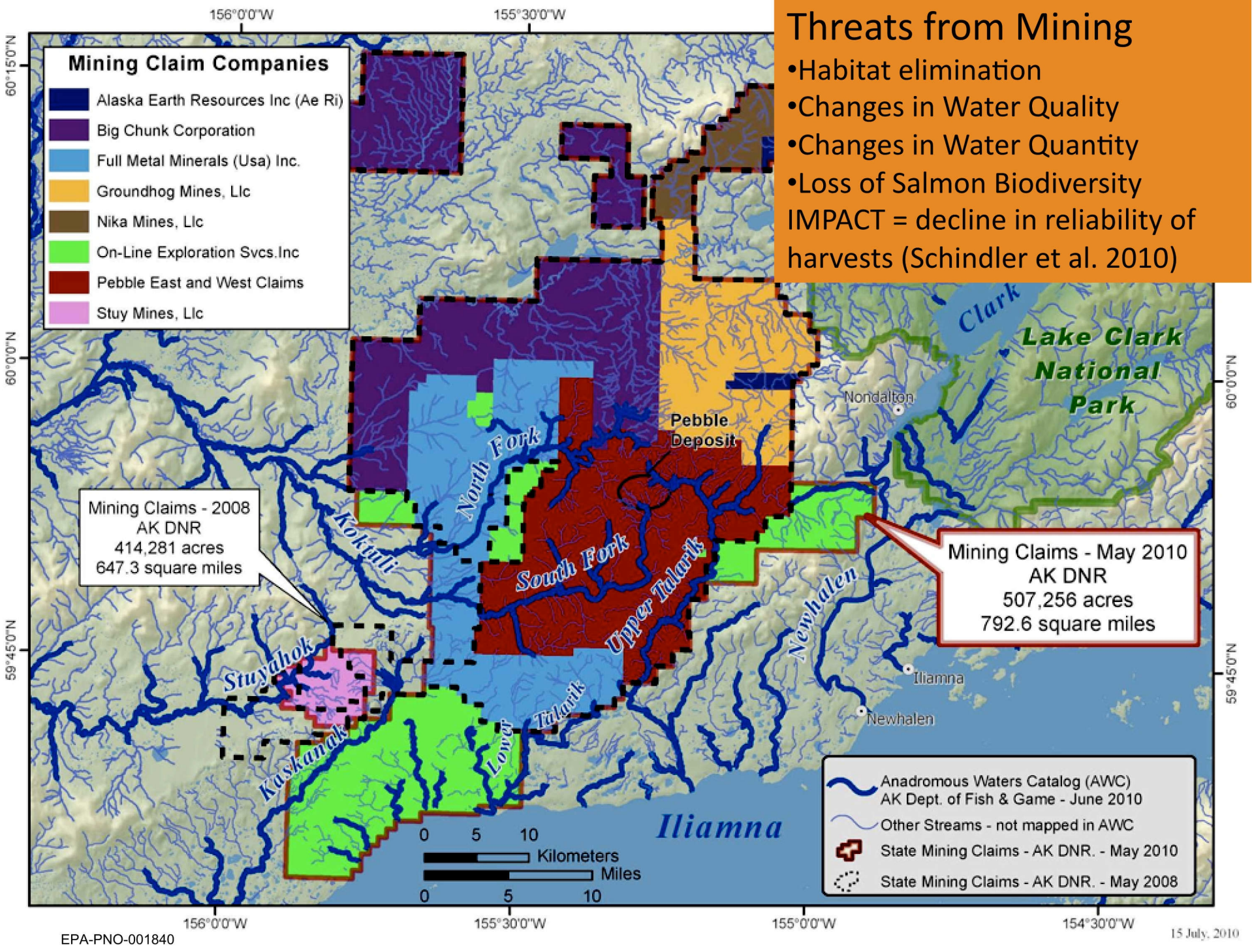
- Second least abundant Pacific salmon species in AK & US (Quinn 2005)
- Alaska represents 50% species range
- Occupy widest array of freshwater habitat ranging from large fourth order rivers to first order headwater streams. Rear 1-3 years in small streams.
- In Bristol Bay, spawn later than other salmon species, during more inclement weather which poses logistical challenges for studies (Price & Larson 1999, Dion & Hetrick 2006)
- Few Bristol Bay coho studies.

Tributary to S. Fork Koktuli

Bristol Bay Coho Salmon Harvest

- Commercial (Jones et al. 2012)
  - AVG harvest = 84,335 (1991-2010)
  - 2011 harvest ~ 108,000
- Sport (ADFG Sport Fish 2011 data)
  - 20,706 anglers fished 98,522 day
  - top 3 species harvested were: **coho** (16,045), sockeye (15,232) & Chinook (10,897)
- Subsistence (ADFG Subsistence Div.)
  - ALL communities use coho salmon
  - Average harvest/household/all years = 108.3 lbs

CSP2



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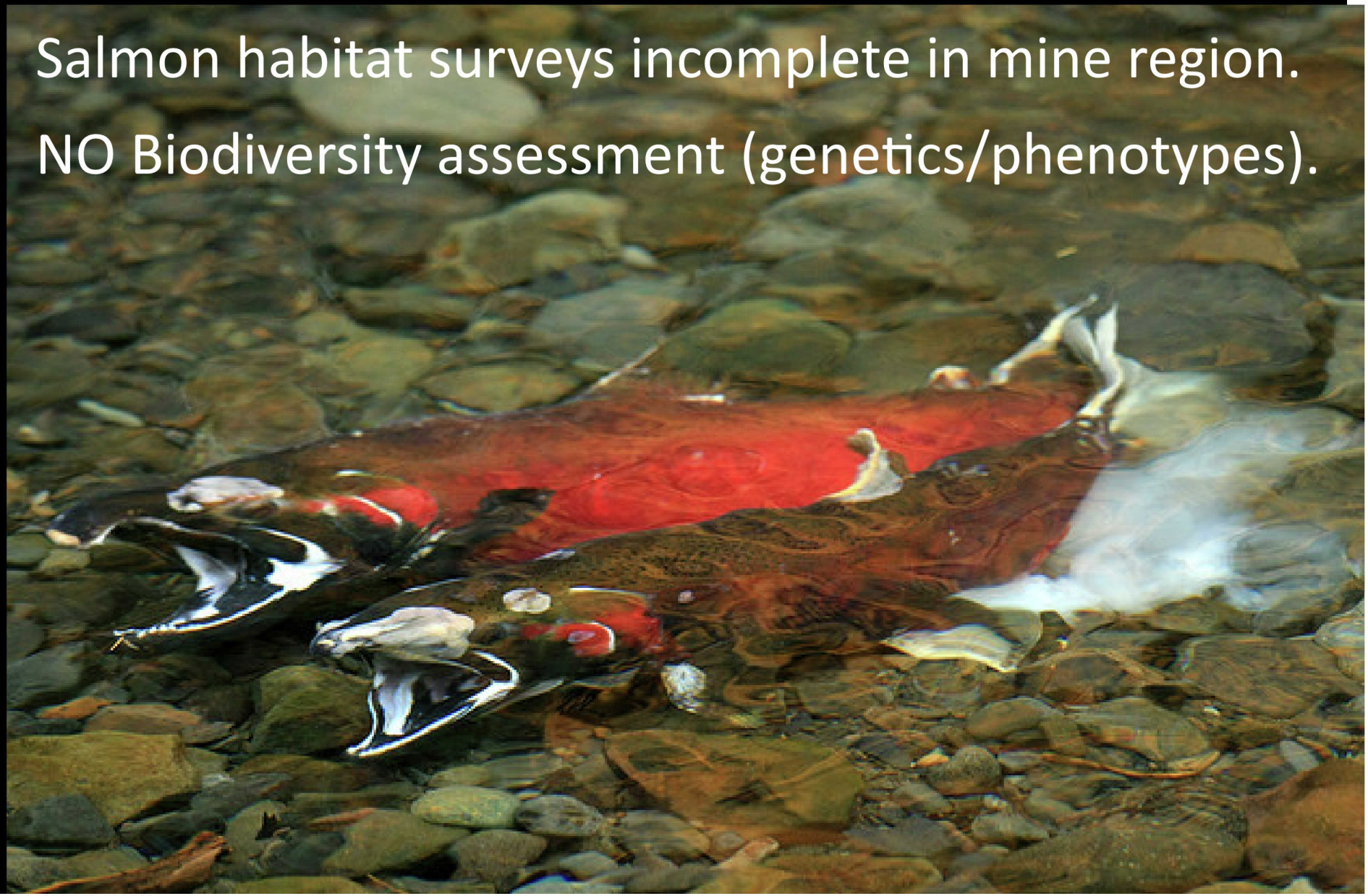
Lack of Data on Coho in Proposed Mine Region

- Salmon habitat surveys incomplete in mine region.
- NO Biodiversity assessment (genetics/phenotypes).



Available Habitat Data in & near Mine District

- In low order, wadeable streams < 10% gradient juvenile coho documented in 75% of streams (n=105) in and near proposed mining district (Woody and O'Neal 2011)
- O'Neal and Woody (submitted). In low order streams, coho occurred at second highest densities 0.38 ± 0.08 coho/m^2 (n=12) next to sculpin.

Available coho salmon biodiversity: Genotypes

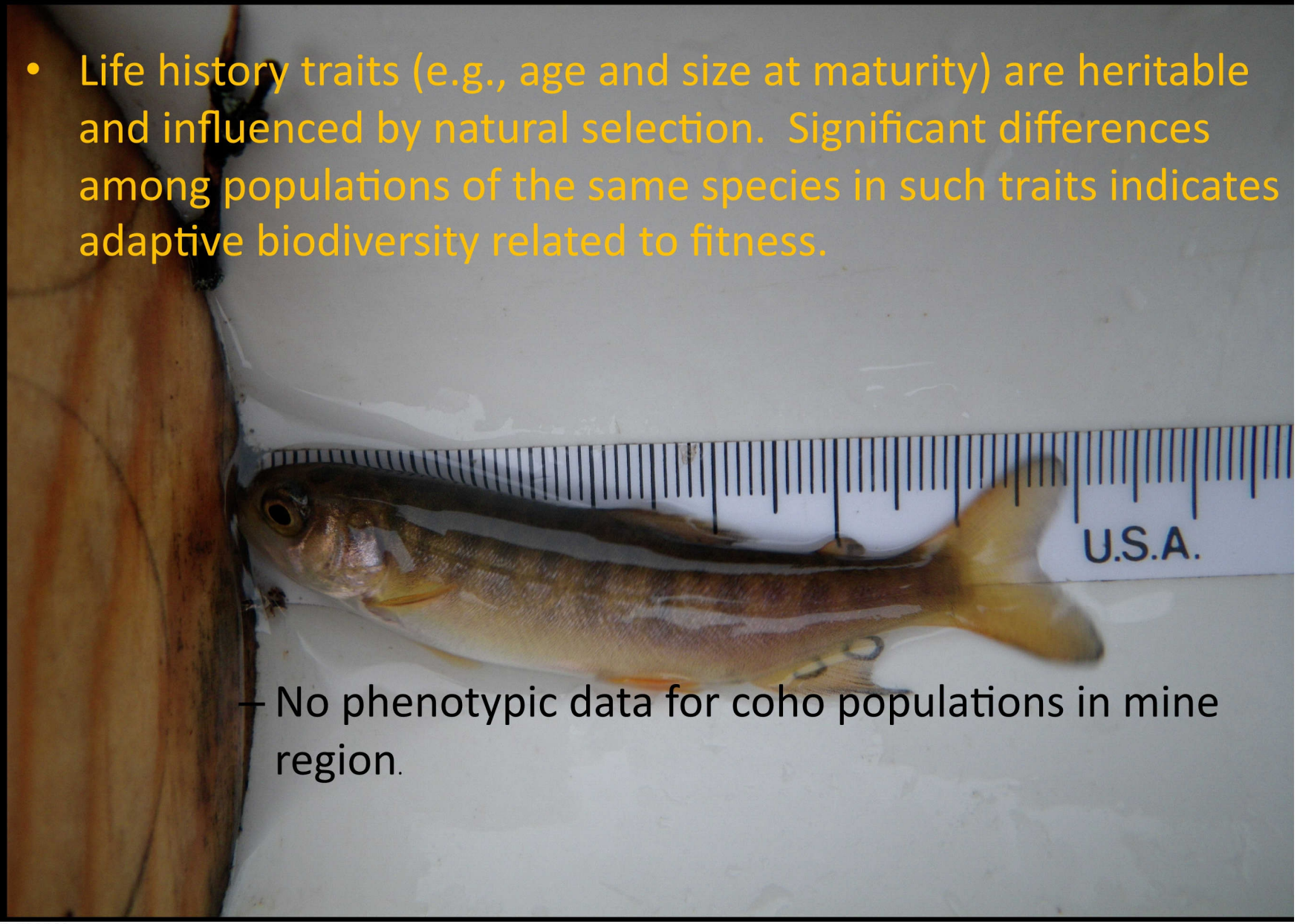
NO studies in or near mine district.

BUT 3 Important Alaska Studies:

- **Olsen et al. 2003**. Conservation genetics. 4:557-569.
- **Olsen et al. 2004**. TAFS. 133:476-483.
- **Olsen et al. 2011**. Conservation Genetics. 12:223-241.

These studies indicate Alaskan coho spawning populations tend to be small & genetically distinct, more so than other salmon species. As such coho are at relatively higher risk of genetic diversity loss and extirpation due to habitat loss than chum and Chinook salmon.

Available Coho Salmon Biodiversity: Phenotypes



- Life history traits (e.g., age and size at maturity) are heritable and influenced by natural selection. Significant differences among populations of the same species in such traits indicates adaptive biodiversity related to fitness.
  - No phenotypic data for coho populations in mine region.

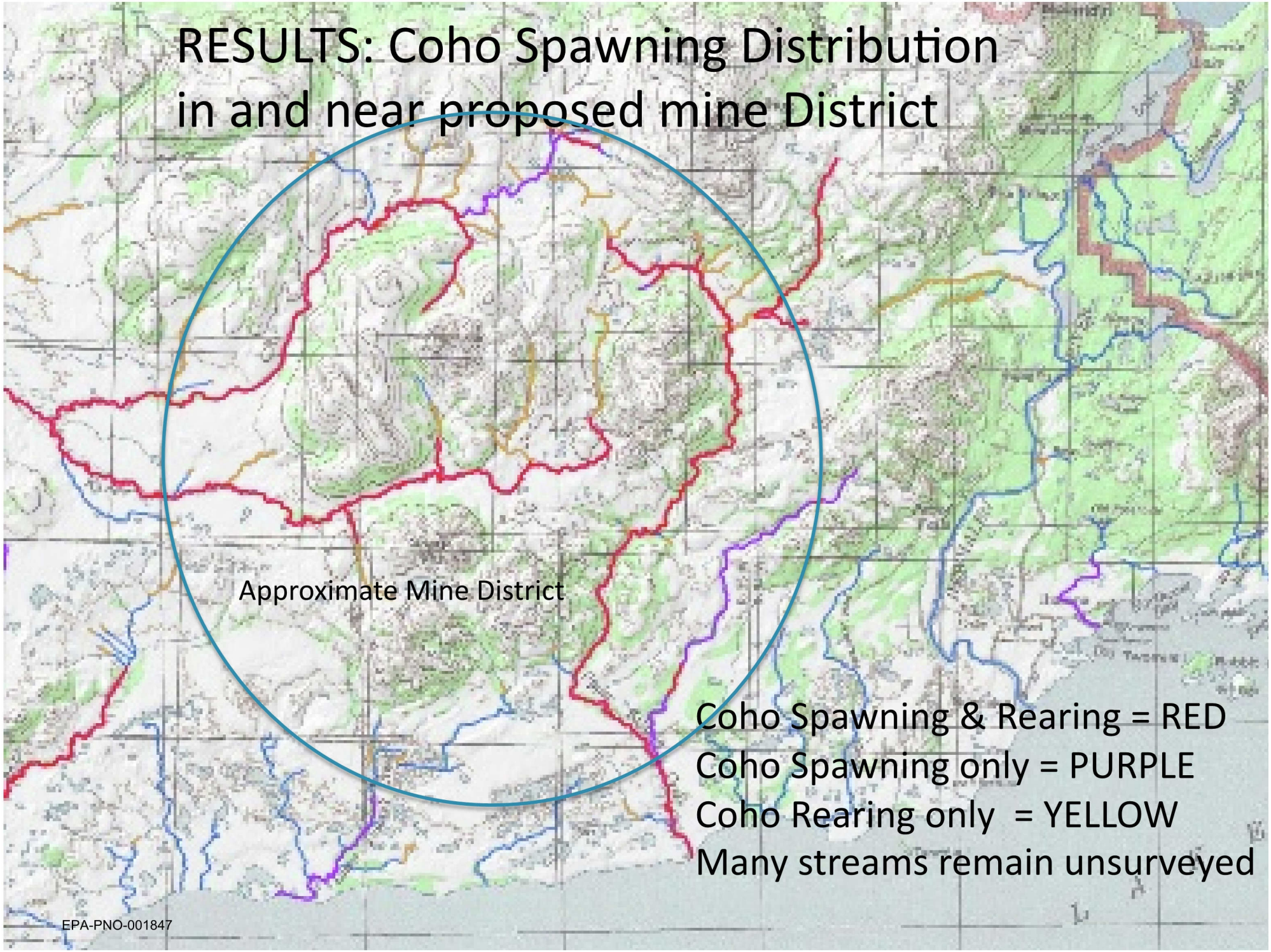
Methods:

- Coho spawning habitat documentation
  - Conducted low level (50-150 m) helicopter surveys for spawning/migrating coho during 2009, 2011
  - Georeferenced (GPS) spawning & migrating coho
  - Nominated spawning habitat to ADFG Anadromous Waters Catalog (AWC).
  - Mapped using AWC ARCINFO database (ADFG 2013).

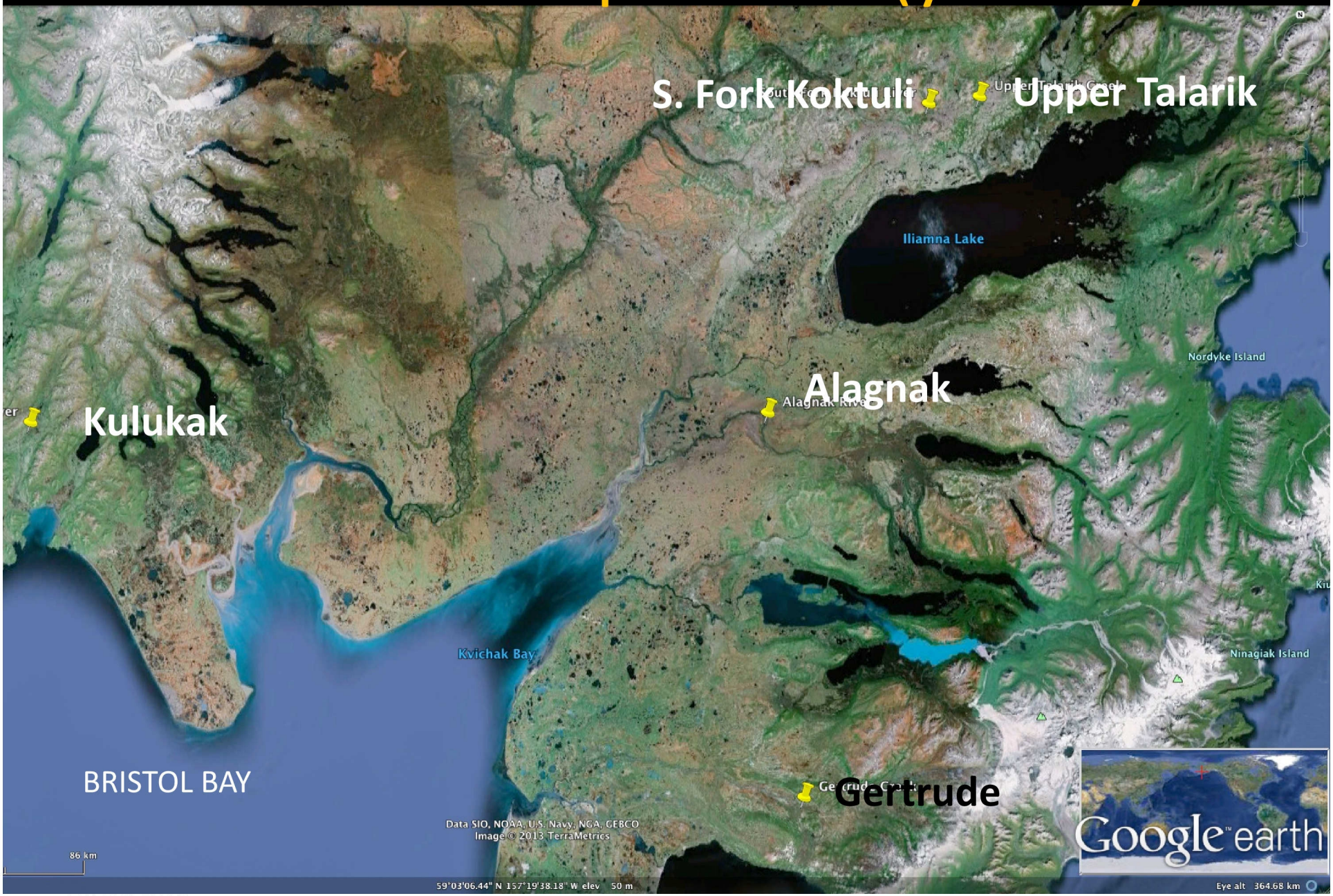
Methods

Biodiversity

- Genotypic – 8 micro-satellite loci from S. Fork Koktuli (Nushagak) & Upper Talarik Creek (Kvichak)
- Phenotypic – Age & size at maturity, collected & analyzed scales for age, surveyed for length (MEH) & depth.


RESULTS: Coho Spawning Distribution
in and near proposed mine District
Approximate Mine District
Coho Spawning & Rearing = RED
Coho Spawning only = PURPLE
Coho Rearing only = YELLOW
Many streams remain unsurveyed
EPA-PNO-001847

Genetic Sample Sites (yellow)



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Genotypic comparison of 8 microsatellite loci among 5 Bristol Bay coho populations. Data from US Fish and Wildlife Service Conservation Genetics Lab, Anchorage, AK.

System	Tributary	Code	Year	n
Alagnak River	Alagnak River	ALAG	1997	89
King Salmon River	Gertrude Creek	GERT	1997	96
Nushagak River	South Fork Koktuli River	HSKA	2011	78
Kvichak River	Upper Talarik Creek	HUTA	2011	73
Kulukak River	Kulukak River	KULU	1997	91

microsatellite loci analyzed = Oke2, Oke3, Oke4, Oki1, Oki 3, Oki11, Oneu3, Ots105
No significant departures observed from HW equilibrium, therefore populations were compared using GENEPOP & Fstat

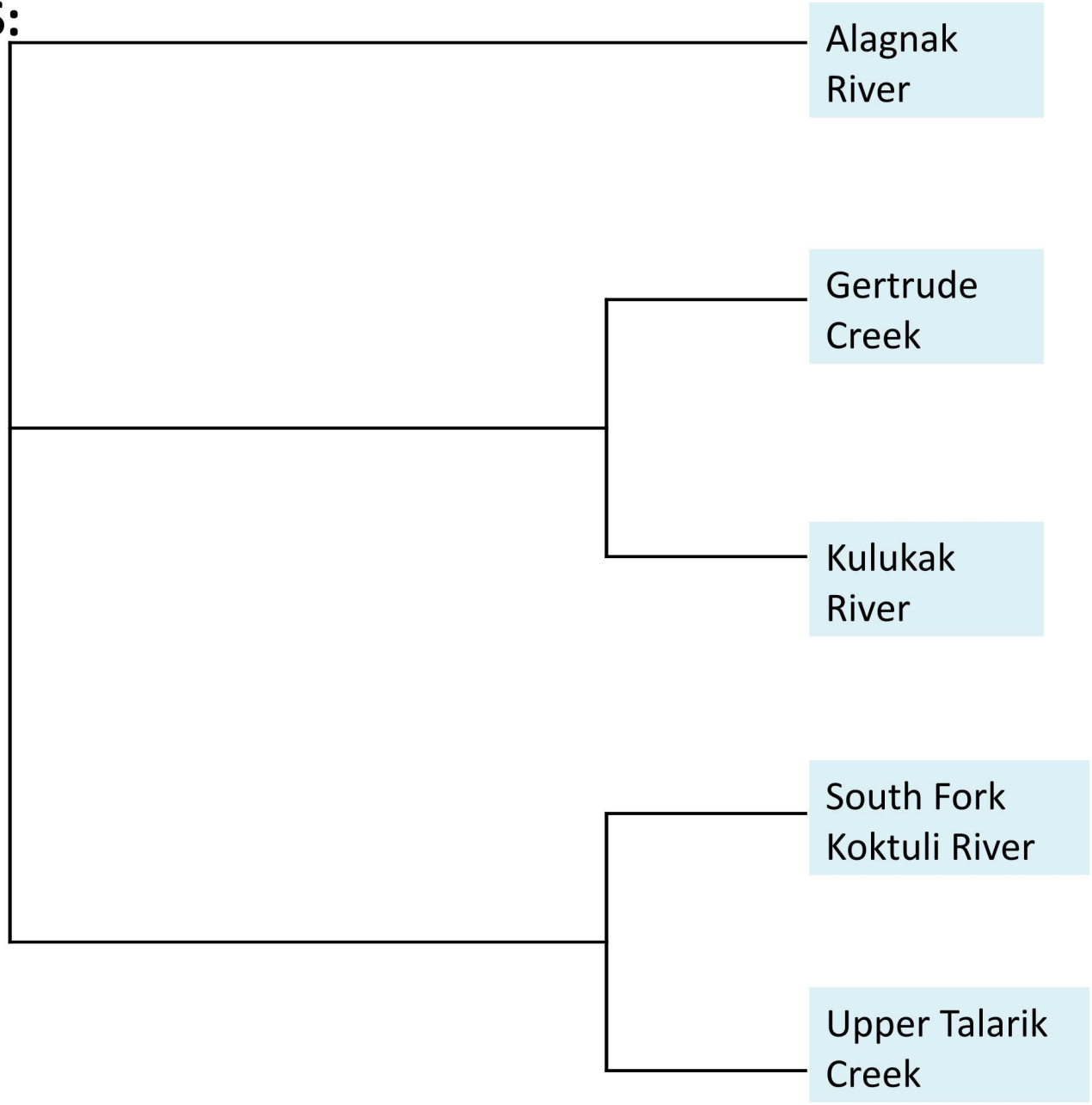
BIODIVERSITY RESULTS:

Genotypic

All spawning populations differed significantly from each other (Fst p = 0.026; 99% CI = 0.014- 0.044)

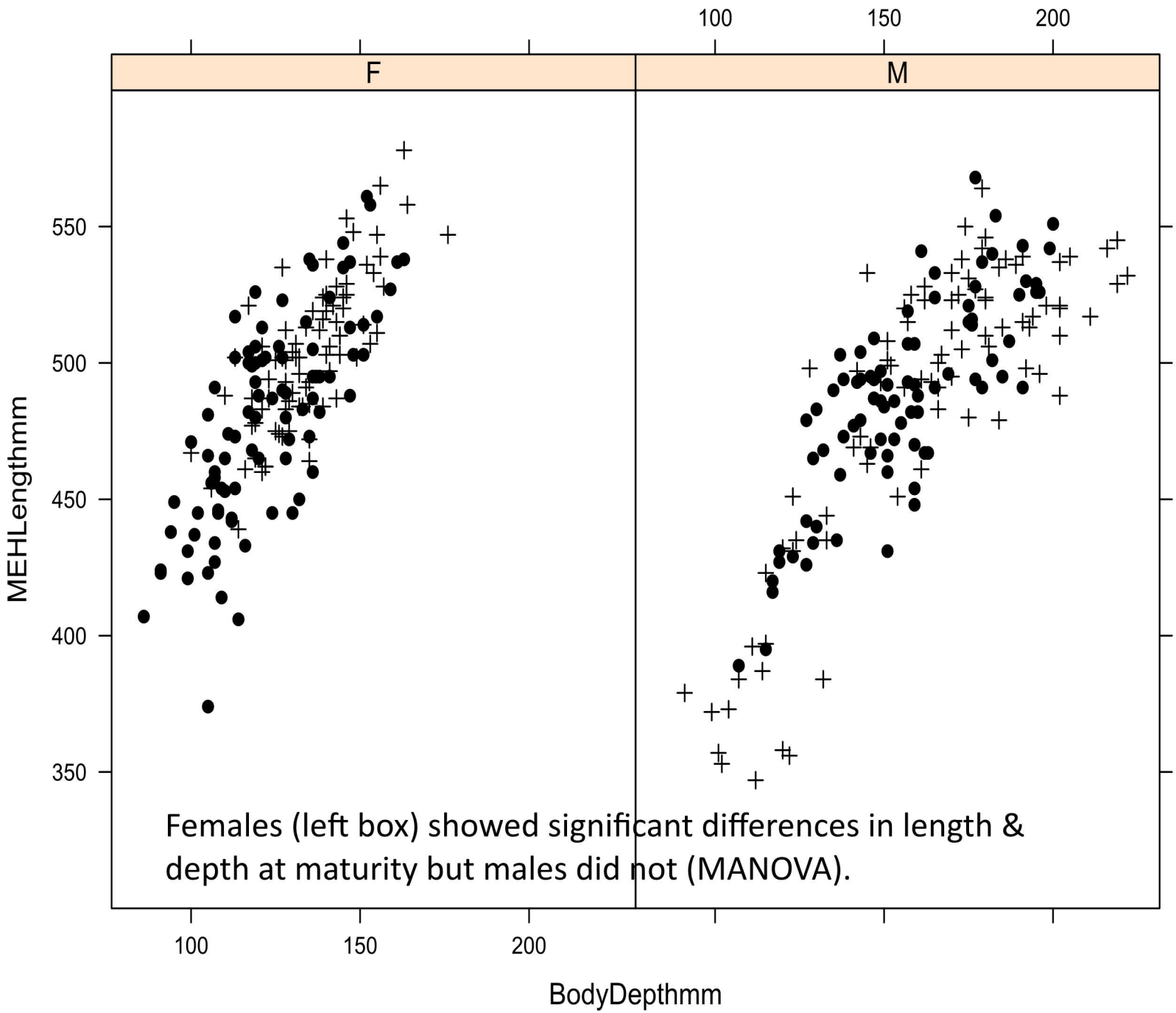
This phenogram (PHYLIP) shows grouping based on genetic analysis.

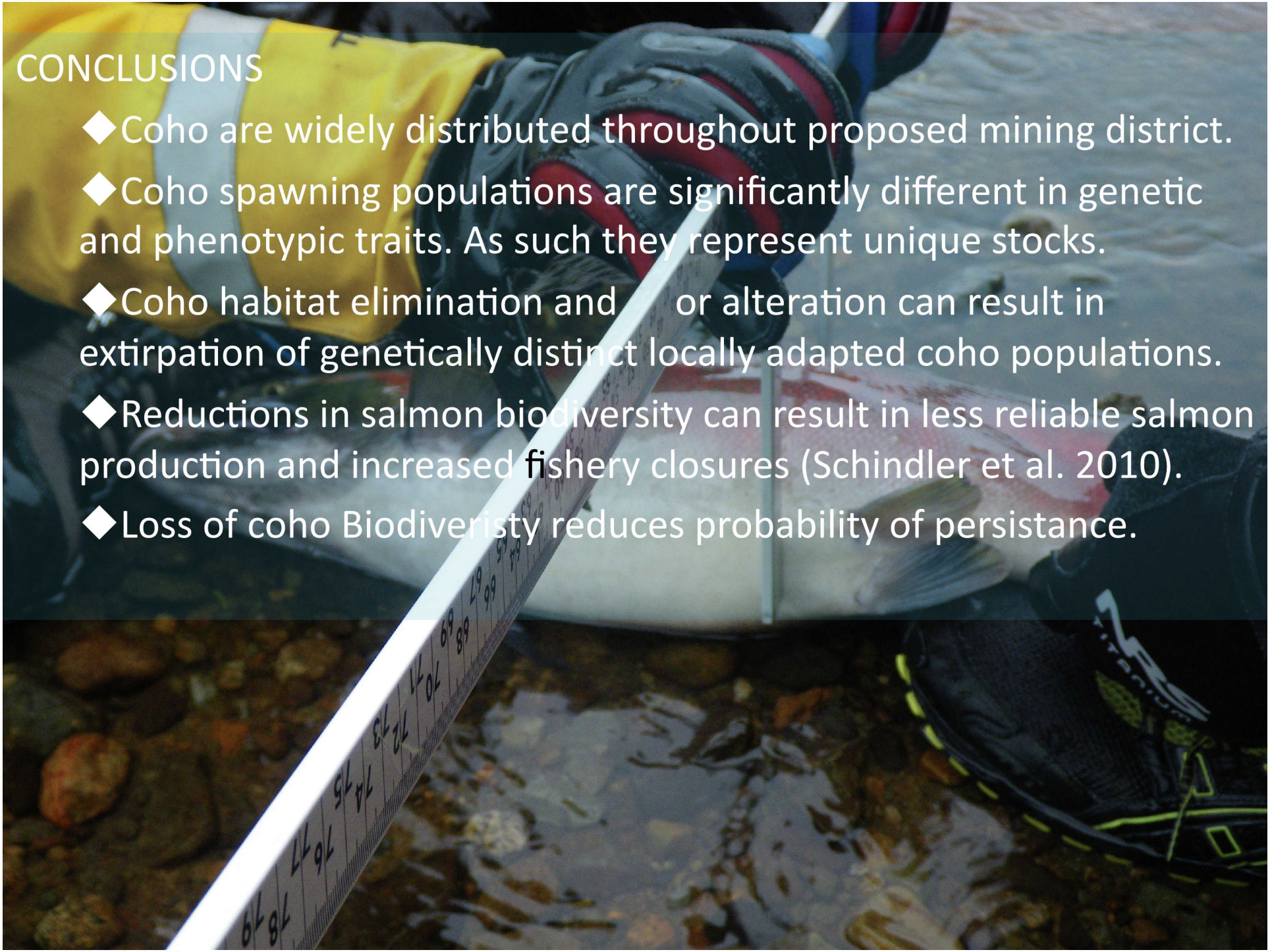
BOTTOM LINE:
ALL surveyed coho populations in Bristol Bay are genetically unique. Habitat elimination would result in elimination of unique genetic diversity.



BIODIVERSITY RESULTS: Phenotypic

- Significant differences between male age distribution (Pearsons Chi Square test; p = 0.007); more 1. observed in S. Fork Koktuli than expected and more 2. observed in Upper Talarik than expected.
- Females showed no significant differences in age distribution among sites BUT…
- Females showed significant differences in length and depth at maturity, males did not (MANOVA w/ Pillai-Bartlett statistic (Krzanowski 1988).


F
M
100
150
200
550
500
450
400
350
MEHLengthmm
BodyDepthmm
Females (left box) showed significant differences in length & depth at maturity but males did not (MANOVA).



CONCLUSIONS

- Coho are widely distributed throughout proposed mining district.
- Coho spawning populations are significantly different in genetic and phenotypic traits. As such they represent unique stocks.
- Coho habitat elimination and or alteration can result in extirpation of genetically distinct locally adapted coho populations.
- Reductions in salmon biodiversity can result in less reliable salmon production and increased fishery closures (Schindler et al. 2010).
- Loss of coho Biodiveristy reduces probability of persistance.